WHAT IS CLAIMED IS:

1. An isolated polynucleotide selected from: (a) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof; (b) a polynucleotide comprising a portion at least 300 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2 or 4; (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant; (f) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide hybridises to the sequence of (a), (b), (c), (d), (e) or to a complement thereof, under at least low stringency conditions; and (g) a polynucleotide comprising a portion at least 15 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3, or of a complement of that sequence, wherein the portion hybridises to a sequence of (a), (b), (c), (d), (e) or to a complement thereof, under at least low stringency conditions.

2. A nucleic acid construct, comprising a polynucleotide according to claim 1 operably connected to a regulatory element, which is operable in the plant.

3. A nucleic acid construct according to claim 2, wherein the construct is a vector.

4. An isolated host cell containing a nucleic acid construct according to claim 2.

5. A host cell according to claim 4, wherein the host cell is a plant cell.

6. A host cell according to claim 5, wherein the plant cell has the nucleic acid construct incorporated into its nucleome.

7. A host cell according to claim 5, wherein the plant cell has the nucleic acid construct stably incorporated into its genome.

8. A plant containing a cell comprising a nucleic acid construct according to claim 2.

9. A plant according to claim 8, wherein the plant cell has the nucleic acid construct stably incorporated into its genome.

10. A probe for interrogating nucleic acid for the presence of a disease resistance-conferring polynucleotide or portion thereof, the probe comprising a nucleotide sequence that hybridises under at least low stringency conditions to a polynucleotide according to claim 1.

11. A probe according to claim 10, wherein the probe essentially of a nucleic acid sequence which corresponds or is complementary to at least a portion of a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion is at least 15 nucleotides in length.

12. A probe according to claim 10, wherein the probe comprises a nucleotide sequence that is capable of hybridising to at least a portion of a nucleotide sequence encoding the amino acid sequence set forth in SEQ ID NO: 2 or 4 under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length.

13. A probe according to claim 10, wherein the probe comprises a nucleotide sequence that is capable of hybridising to at least a portion of SEQ ID NO: 1 or 3 under at least low stringency conditions, wherein the portion is at least 15 nucleotides in length.

14. A method for modulating disease resistance in a plant, the method comprising introducing a construct into the nucleome of the plant and regenerating a stably transformed plant, the construct comprising a regulatory element operably connected to a polynucleotide selected from: (a) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof; (b) a polynucleotide comprising a portion at least 300 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2 or 4; (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant and (f) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide hybridises to the sequence of (a), (b), (c), (d), (e) or to a complement thereof, under at least low stringency conditions

15. A method according to claim 14, wherein the construct is introduced into regenerable plant cells so as to yield transformed plant cells.

16. A method according to claim 15, wherein the transformed plant cells are used for regenerating a differentiated plant.

17. A method according to claim 15, wherein the regenerable cells are regenerable dicotyledonous plant cells.

18. A method according to claim 15, wherein the regenerable cells are regenerable monocotyledonous plant cells.

19. A method according to claim 15, wherein regenerable cells are regenerable graminaceous monocotyledonous plant cells.

20. A method according to claim 15, wherein regenerable cells are regenerable non-graminaceous monocotyledonous plant cells.

21. A method according to claim 15, wherein regenerable cells are regenerable banana cells.

22. A method according to claim 16, wherein the expression of the polynucleotide renders the differentiated transgenic plant with enhanced resistance to disease.

23. A method according to claim 22, wherein disease is caused by a fungal pathogen.

24. A method according to claim 22, wherein disease is caused by soil borne fungi.

25. A method according to claim 22, wherein disease is caused by *Fusarium* species.

26. A method according to claim 16, wherein the nucleic acid construct is transmitted through a complete cycle of the differentiated transgenic plant to its progeny so that it is expressed by the progeny plants.

27. A method according to claim 26, wherein the progeny is selected from seed, plant parts, tissue, and progeny plants derived from the differentiated transgenic plant.

28. A method of breeding a plant, the method comprising transferring from a plant genetic material corresponding to a polynucleotide *via* crossing and backcrossing to another plant, wherein the polynucleotide is selected from: (a) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide conferring disease resistance to a plant, the sequence sharing at least 30% sequence identity with the sequence set forth in SEQ ID NO: 1 or 3, or a complement thereof; (b) a polynucleotide comprising a portion at least 300 contiguous nucleotides in length of the sequence set forth in SEQ ID NO: 1 or 3 or of a complement of that sequence, wherein the portion encodes a polypeptide that confers disease resistance to a plant; (c) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 2 or 4; (d) a polynucleotide comprising a nucleotide sequence that encodes a portion at least 100 contiguous amino acid residues in length of the amino acid sequence set forth in SEQ ID NO: 2 or 4, wherein the portion confers disease resistance to a plant; (e) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that shares at least 50% sequence similarity with at least a portion at least 300 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant and (f) a polynucleotide comprising a nucleotide sequence that encodes a polypeptide that confers disease resistance to a plant, wherein the polynucleotide hybridises to the sequence of (a), (b), (c), (d), (e) or to a complement thereof, under at least low stringency conditions.

29. A method according to claim 28, wherein the other plant is susceptible to a pathogenic disease.

30. A method according to claim 29, wherein the disease is caused by a fungal pathogen.

31. A method according to claim 29, wherein the disease is caused by a *Fusarium* species.

32. A method according to claim 28, wherein the genetic material comprises naturally-occurring DNA.

33. A method according to claim 28, comprising: (1) sexually crossing a plant containing the genetic material with a plant from a pathogen susceptible taxon; (2) recovering reproductive material from the progeny of the cross; and (3) growing plants with enhanced resistance to the disease from the reproductive material.

34. A method according to claim 33, further comprising prior to step (1): identifying a plant that is resistant to the pathogenic disease by detecting expression in the plant of the polynucleotide.

35. A method according to claim 33, further comprising repetitively: (a) backcrossing the disease resistant progeny with disease susceptible plants from the susceptible taxon; and (b) selecting for expression of a nucleic acid sequence corresponding to the polynucleotide or to marker gene associated with the polynucleotide among the progeny of the backcross, until the desired characteristics of the susceptible taxon are present in the progeny.

36. An isolated polypeptide selected from: (i) a polypeptide comprising an amino acid sequence that shares at least 50% similarity with the sequence set forth in SEQ ID NO: 2 or 4; (ii) a polypeptide comprising a portion at least 100 contiguous amino acid residues in length of the sequence set forth in SEQ ID NO: 2 or 4, wherein the polypeptide confers disease resistance to a plant; (iii) a polypeptide comprising an amino acid sequence that shares at least 30% similarity with at least a portion of the sequence set forth in SEQ ID NO: 2 or 4, wherein the portion is at least 100 contiguous amino acid residues in length; and (iv) a polypeptide comprising at least a portion of of the sequence set forth in SEQ ID NO: 2 or 4, wherein the portion is at least 5 contiguous amino acid residues in length and is immuno-interactive with an antigen-binding molecule that is immuno-interactive with a sequence selected from (i), (ii) or (iii).

37. A polypeptide according to claim 36, wherein the polypeptide comprises at least one domain selected from:

(a) a domain which corresponds to residues 1-167 of Figure 2;

(b) a domain which corresponds to residues 168-536 of Figure 2; and

(c) a domain which corresponds to residues 537-1476 of Figure 2;

38. A polypeptide according to claim 37, wherein the domain defined in (a) is structurally similar to a coiled coil.

39. A polypeptide according to claim 37, wherein the domain defined in (a) has at least 60% sequence similarity with, or at least 30% sequence identity to, or differs at no more than 40 amino acid residues from, the corresponding domain of in Figure 2.

40. A polypeptide according to claim 37, wherein the domain defined in (a) comprises a sequence according to Formula (I):

Ser-Φaa_1-Φaa_2 Zaa-Xaa_1-Φaa_3-Φaa_4 Xaa_2-Baa_1 Σaa_1-Xaa_3-Asn-Xaa_4-Xaa_5-Φaa_5-Xaa_6-Xaa_7-Leu-Xaa_8-Xaa_9-Xaa_{10}-Xaa_{11}-Xaa_{12}-Xaa_{13}-Baa_2-Xaa_{14}-$Åaa_1$-Leu-Xaa_{15}-Xaa_{16}-Leu-Xaa_{17}-Xaa_{18}-Σaa_2-Leu-Leu-Arg-Xaa_{19}-His-Σaa_3-Φaa_6-Leu-$Åaa_2$-Ωaa_1-Ala-Ωaa_2-Σaa_4-Arg-Xaa_{20}-Xaa_{21}-Xaa_{22}-Xaa_{23}-Xaa_{24}-Xaa_{25}-Xaa_{26}-Ser-Leu-Val-Xaa_{27}-Φaa_7-Φaa_8-Xaa_{28}-Xaa_{29}-Leu-Lys-$Åaa_3$-Xaa_{30}-Ala-Tyr-Asp-Ala-$Åaa_4$-Asp-Φaa_9-Leu-$Åaa_5$-Glu-Φaa_{10}-Glu-Xaa_{31}-Xaa_{32}-Ala-Xaa_{33}-Baa_3-Xaa_{34}-Lys-Val (I)

wherein: each of Φ_{1-10} is independently selected from any hydrophobic amino acid residue,
Zaa is a neutral/polar amino acid residue,
each of Σaa_{1-4} is independently selected from any small amino acid residue,
each of Baa_{1-3} is independently selected from any basic amino acid residue,
each of $Åaa_{1-5}$ is independently selected from any acidic amino acid residue,
each of Ωaa_{1-2} is independently selected from any charged amino acid residue, and
Xaa_{1-33} are each independently selected from any amino acid residue.

41. A polypeptide according to claim 37, wherein the domain defined in (b) is functionally analogous to a nuclear-binding site (NBS) domain.

42. A polypeptide according to claim 37, wherein the domain defined in (b) has at least 70% sequence similarity with, or at least 50 90% sequence identity to, or differs at no more than 40 amino acid residues from, the corresponding domain in Figure 2.

43. A polypeptide according to claim 37, wherein the domain defined in (b) comprises a sequence according to Formula (II):

Arg-Xaa_1-Xaa_2-Thr-Σaa_1-Ser-Φaa_1-Leu-Thr-Glu-Σaa_2-Xaa_3-Φaa_2-Φaa_3-Gly-Arg-Xaa_4-Gln-$Åaa_1$-Baa_1-Glu-Xaa_5-Φaa_4-Φaa_5-Ωaa_1-Leu-Leu-Leu-$Åaa_2$-Σaa_3-Σaa_4-Xaa_6-Gly-Xaa_7-Xaa_8-Σaa_5-Phe-Σaa_6-Val-Φaa_6-Pro-Φaa_7-Val-Gly-Φaa_8-Gly-Gly-Xaa_9-Gly-Lys-Thr-Thr-Leu-Σaa_7-Gln-Leu-Φaa_9-Φaa_{10}-Asn-Asp-Xaa_{10}-Arg-Val-Xaa_{11}-Xaa_{12}-Xaa_{13}-Phe-Xaa_{14}-Leu-Baa_2-Φaa_{11}-Trp-Val-Cys-Val-Ser-Asp-Xaa_{15}-Phe-Xaa_{16}-Val-Lys-Arg-Φaa_{12}-Thr-Baa_3-Glu-Ile-Xaa_{17}-Glu-Xaa_{18}-Ala-Thr-Xaa_{19}-Xaa_{20}-Ωaa_2-Xaa_{21}-Xaa_{22}-Asp-Xaa_{23}-Xaa_{24}-Asn-Leu-Xaa_{25}-Xaa_{26}-Leu-Gln-Xaa_{27}-Xaa_{28}-Leu-Lys-Glu-Ωaa_3-Ile-Xaa_{29}-Σaa_8-Xaa_{30}-Xaa_{31}-Phe-Leu-Leu-Val-Leu-Asp-Asp-Val-Trp-Xaa_{32}-Glu-Xaa_{33}-Xaa_{34}-Xaa_{35}-Ωaa_4-Trp-Glu-Xaa_{36}-Leu-Xaa_{37}-Ala-Pro-Leu-Ωaa_5-Xaa_{38}-Σaa_9-Σaa_{10}-Arg-Gly-Ser-Xaa_{39}-Val-Ile-Val-Thr-Thr-Xaa_{40}-Xaa_{41}-Xaa_{42}-Lys-Φaa_{13}-Ala-Xaa_{43}-Φaa_{14}-Xaa_{44}-Gly-Thr-Met-Ωaa_6-Xaa_{45}-Φaa_{15}-Xaa_{46}-Leu-$Åaa_3$-Xaa_{47}-Leu-Xaa_{48}-$Åaa_4$-Asp-Xaa_{49}-Xaa_{50}-Trp-Xaa_{51}-Leu-Φaa_{16}-Ωaa_7-Xaa_{52}-Xaa_{53}-Σaa_{11}-Phe-Xaa_{54}-Xaa_{55}-Xaa_{56}-Xaa_{57}-Xaa_{58}-Σaa_{12}-Xaa_{59}-Xaa_{60}-Xaa_{61}-Xaa_{62}-Ωaa_8-Φaa_{17}-Glu-Xaa_{63}-Ile-Gly-Arg-Lys-Ile-Ala-Xaa_{64}-Lys-Φaa_{18}-Xaa_{65}-Gly-Xaa_{66}-Pro-Φaa_{19}-Σaa_{13}-Ala-Xaa_{67}-Σaa_{14}-Φaa_{20}-Gly-Xaa_{68}-Φaa_{21}-Leu-Arg-Xaa_{69}-Ωaa_9-Xaa_{70}-Σaa_{15}-Xaa_{71}-Xaa_{72}-Xaa_{73}-Trp-Arg-Xaa_{74}-Φaa_{22}-Φaa_{23}-Glu-Σaa_{16}-Glu-Xaa_{75}-Trp-Xaa_{76}-Φaa_{24}-Pro-Xaa_{77}-Ala-Xaa_{78}-Xaa_{79}-$Åaa_5$-Φaa_{25}-Leu-Σaa_{17}-Xaa_{80}-Leu-Xaa_{81}-Xaa_{82}-Ser-Tyr-Xaa_{83}-Xaa_{84}-Leu-Pro-Σaa_{18}-Xaa_{85}-Leu-Baa_4-Xaa_{86}-Cys-Phe-Ala-Phe-Cys-Ala-Φaa_{26}-

Phe-Xaa_{87}-Lys-Xaa_{88}-Tyr-Xaa_{89}-Phe-Xaa_{90}-Lys-Ωaa_{10}-Xaa_{91}-Leu-Ile-Xaa_{92}-Xaa_{93}-Trp-Ile-Ala-Xaa_{94}-Xaa_{95}-Φaa_{27}-Ile (II)

wherein: each of Φ_{1-27} is independently selected from any hydrophobic amino acid residue,
each of Σaa_{1-18} is independently selected from any small amino acid residue,
each of Baa_{1-4} is independently selected from any basic amino acid residue,
each of $\mathring{A}aa_{1-5}$ is independently selected from any acidic amino acid residue,
each of Ωaa_{1-10} is independently selected from any charged amino acid residue, and
Xaa_{1-95} are each independently selected from any amino acid residue.

44. A polypeptide according to claim 37, wherein the domain defined in (c) is functionally analogous to a leucine-rich repeat (LRR) domain.

45. A polypeptide according to claim 37, wherein the domain defined in (c) has at least 60% sequence similarity with, or at least 30% sequence identity to, or differs at no more than 40 amino acid residues from, the corresponding domain in Figure 2.

46. A polypeptide according to claim 37, wherein the domain defined in (b) comprises a sequence according to Formula (III):

Leu-Xaa_1-Ωaa_1-Xaa_2-Φaa_1-Phe-Baa_1-Xaa_3-Leu-Xaa_4-Arg-Ile-Baa_2-Val-Leu-Xaa_5-Φaa_2-Xaa_6-Xaa_7-Cys-Xaa_8-Φaa_3-Baa_3-Xaa_9-Leu-Pro-Xaa_{10}-Xaa_{11}-Φaa_4-Gly-Xaa_{12}-Leu-Xaa_{13}-Xaa_{14}-Leu-Arg-Tyr-Leu-Xaa_{15}-Φaa_5-Ser-Xaa_{16}-Asn-Σaa_1-Xaa_{17}-Ile-Gln-Arg-Leu-Pro-Glu-Ser-Φaa_6-Xaa_{18}-Ωaa_2-Leu-Xaa_{19}-Xaa_{20}-Leu-Gln-Σaa_2-Leu-Xaa_{21}-Leu-Xaa_{22}-Gly-Cys-Xaa_{23}-Leu-Xaa_{24}-Xaa_{25}-Φaa_7-Pro-Xaa_{26}-Σaa_3-Met-Ser-Baa_4-Leu-Φaa_8-Xaa_{27}-Leu-Arg-Gln-Leu-Baa_5-Xaa_{28}-Xaa_{29}-Xaa_{30}-$\mathring{A}aa_1$-Φaa_9-Ile-Σaa_4-Ωaa_3-Ile-Xaa_{31}-Ωaa_4-Val-Gly-Baa_6-Leu-Ile-Xaa_{32}-Leu-Gln-Glu-Leu-Xaa_{33}-Ala-Φaa_{10}-Xaa_{34}-Val-Xaa_{35}-Xaa_{36}-Baa_7-Xaa_{37}-Gly-Xaa_{38}-Xaa_{39}-Φaa_{11}-Ala-Glu-Leu-Ser-Σaa_5-Φaa_{12}-Xaa_{40}-Gln-Leu-Baa_8-Σaa_6-Xaa_{41}-Leu-Xaa_{42}-Ile-Xaa_{43}-Asn-Leu-Xaa_{44}-Asn-Val-Xaa_{45}-Xaa_{46}-Xaa_{47}-Ωaa_5-Glu-Σaa_7-Xaa_{48}-Lys-Ala-Baa_9-Leu-Ωaa_6-Ωaa_7-Lys-Gln-Xaa_{49}-Leu-Ωaa_8-Xaa_{50}-Leu-$\mathring{A}aa_2$-Leu-Ωaa_9-Trp-Ala-Xaa_{51}-Gly-Xaa_{52}-Xaa_{53}-Xaa_{54}-Xaa_{55}-Xaa_{56}-Xaa_{57}-Xaa_{58}-Glu-Xaa_{59}-Xaa_{60}-Xaa_{61}-Xaa_{62}-Ωaa_{10}-Ωaa_{11}-Val-Leu-Xaa_{63}-Gly-Leu-Xaa_{64}-Pro-His-Xaa_{65}-Xaa_{66}-Leu-Baa_{10}-Xaa_{67}-Leu-Σaa_8-Ile-Baa_{11}-Xaa_{68}-Tyr-Σaa_9-Gly-Σaa_{10}-Σaa_{11}-Xaa_{69}-Pro-Ser-Trp-Φaa_{13}-Xaa_{70}-Xaa_{71}-Xaa_{72}-Φaa_{14}-Leu-Pro-Asn-Φaa_{15}-Xaa_{73}-Thr-Φaa_{16}-Baa_{12}-Leu-Ωaa_{12}-Xaa_{74}-Cys-Σaa_{12}-Arg-Leu-Xaa_{75}-Xaa_{76}-Leu-Σaa_{13}-Xaa_{77}-Φaa_{17}-Gly-Gln-Leu-Xaa_{78}-Xaa_{79}-Leu-Baa_{13}-Xaa_{80}-Leu-His-Φaa_{18}-Ωaa_{13}-Xaa_{81}-Met-Σaa_{14}-Xaa_{82}-Val-Baa_{14}-Gln-Φaa_{19}-Xaa_{83}-Xaa_{84}-Xaa_{85}-Φaa_{20}-Xaa_{86}-Gly-Xaa_{87}-Σaa_{15}-Ωaa_{14}-Xaa_{88}-Xaa_{89}-Xaa_{90}-Phe-Pro-Xaa_{91}-Leu-Glu-Xaa_{92}-Leu-Xaa_{93}-Φaa_{21}-Ωaa_{15}-Ωaa_{16}-Met-Pro-Σaa_{16}-Leu-Ωaa_{17}-Glu-Φaa_{22} (III)

wherein: each of Φ_{1-22} is independently selected from any hydrophobic amino acid residue,
each of Σaa_{1-16} is independently selected from any small amino acid residue,
each of Baa_{1-14} is independently selected from any basic amino acid residue,

each of $Åaa_{1-2}$ is independently selected from any acidic amino acid residue,

each of Ωaa_{1-16} is independently selected from any charged amino acid residue, and

Xaa_{1-93} are each independently selected from any amino acid residue.

47. A polynucleotide comprising a nucleotide sequence encoding a polypeptide according to claim 37.

48. An antigen-binding molecule that is specifically immuno-interactive with a polypeptide according to claim 37.